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RAW SEQUENCE LISTING

DATE: 08/04/2004

PATENT APPLICATION: US/10/828,343

TIME: 12:30:01

Input Set : N:\Crf3\RULE60\10828343.raw

Output Set: N:\CRF4\08042004\J828343.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: FLECKENSTEIN, Bernhard
 3 ALBRECHT, Jens-Christian
 4 NEIPEL, Frank
 5 FRIEDMAN-KIEN, Alvin
 6 HUANG, Yao-Qi

7 (ii) TITLE OF INVENTION: VIRAL INTERLEUKIN-6

8 (iii) NUMBER OF SEQUENCES: 4

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: FOLEY & LARDNER
 11 (B) STREET: 3000 K Street, N.W.
 12 (C) CITY: Washington
 13 (D) STATE: D.C.
 14 (E) COUNTRY: U.S.A.
 15 (F) ZIP: 20007-5109

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Floppy disk
 18 (B) COMPUTER: IBM PC compatible
 19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

21 (vi) CURRENT APPLICATION DATA:

C--> 22 (A) APPLICATION NUMBER: US/10/828,343

C--> 23 (B) FILING DATE: 21-Apr-2004

24 (C) CLASSIFICATION:

C--> 29 (vii) PRIOR APPLICATION DATA:

26 (A) APPLICATION NUMBER: US/09/230,048

27 (B) FILING DATE: 12-Mar-1999

30 (A) APPLICATION NUMBER: WO PCT/EP96/03199

31 (B) FILING DATE: 19-JUL-1996

C--> 32 (viii) ATTORNEY/AGENT INFORMATION:

33 (A) NAME: Granados, Patricia D.

34 (B) REGISTRATION NUMBER: 33,683

35 (C) REFERENCE/DOCKET NUMBER: 058315/0129

C--> 36 (ix) TELECOMMUNICATION INFORMATION:

37 (A) TELEPHONE: (202) 672-5300

38 (B) TELEFAX: (202) 672-5399

39 (2) INFORMATION FOR SEQ ID NO: 1:

40 (i) SEQUENCE CHARACTERISTICS:

41 (A) LENGTH: 612 base pairs

42 (B) TYPE: nucleic acid

43 (C) STRANDEDNESS: double

44 (D) TOPOLOGY: linear

ENTERED

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45 (ii) MOLECULE TYPE: DNA (genomic)
46 (ix) FEATURE:
47 (A) NAME/KEY: CDS
48 (B) LOCATION: 1..612
49 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
50 ATG TGC TGG TTC AAG TTG TGG TCT CTC TTG CTG GTC GGT TCA CTG CTG      48
51 Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Leu Val Gly Ser Leu Leu
52 1 5 10 15
53 GTA TCT GGA ACG CGG GGC AAG TTG CCG GAC GCC CCC GAG TTT GAA AAG      96
54 Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys
55 20 25 30
56 GAT CTT CTC ATT CAG AGA CTC AAT TGG ATG CTA TGG GTG ATC GAT GAA      144
57 Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu
58 35 40 45
59 TGC TTC CGC GAC CTC TGT TAC CGT ACC GGC ATC TGC AAG GGT ATT CTA      192
60 Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu
61 50 55 60
62 GAG CCC GCT GCT ATT TTT CAT CTG AAA CTA CCA GCC ATC AAC GAT ACT      240
63 Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr
64 65 70 75 80
65 GAT CAC TGC GGG TTA ATA GGA TTT AAT GAG ACT AGC TGC CTT AAA AAG      288
66 Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys
67 85 90 95
68 CTC GCC GAT GGC TTT TTT GAA TTC GAG GTG TTG TTT AAG TTT TTA ACG      336
69 Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr
70 100 105 110
71 ACG GAG TTT GGA AAA TCA GTG ATA AAC GTG GAC GTC ATG GAG CTT CTG      384
72 Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu
73 115 120 125
74 ACG AAG ACC TTA GGA TGG GAC ATA CAG GAA GAG CTC AAT AAG CTG ACT      432
75 Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr
76 130 135 140
77 AAG ACG CAC TAC AGT CCA CCC AAA TTT GAC CGC GGT CTA TTA GGG AGG      480
78 Lys Thr His Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg
79 145 150 155 160
80 CTT CAG GGA CTT AAG TAT TGG GTG AGA CAC TTT GCT TCG TTT TAT GTT      528
81 Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val
82 165 170 175
83 CTG AGT GCA ATG GAA AAG TTT GCA GGT CAA GCG GTG CGT GTT TTG GAC      576
84 Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp
85 180 185 190
86 TCT ATC CCA GAC GTG ACT CCT GAC GTC CAC GAT AAG      612
87 Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys
88 195 200
90 (2) INFORMATION FOR SEQ ID NO: 2:
91 (i) SEQUENCE CHARACTERISTICS:
92 (A) LENGTH: 204 amino acids
93 (B) TYPE: amino acid
94 (D) TOPOLOGY: linear

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95 (ii) MOLECULE TYPE: protein

96 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

97 Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Leu Val Gly Ser Leu Leu
98   1           5           10           15
99 Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys
100      20           25           30
101 Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu
102      35           40           45
103 Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu
104      50           55           60
105 Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr
106      65           70           75           80
107 Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys
108      85           90           95
109 Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr
110      100          105          110
111 Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu
112      115          120          125
113 Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr
114      130          135          140
115 Lys Thr His Tyr Ser Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg
116      145          150          155          160
117 Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val
118      165          170          175
119 Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp
120      180          185          190
121 Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys
122      195          200

```

124 (2) INFORMATION FOR SEQ ID NO: 3:

125 (i) SEQUENCE CHARACTERISTICS:

126 (A) LENGTH: 212 amino acids

127 (B) TYPE: amino acid

128 (C) STRANDEDNESS:

129 (D) TOPOLOGY: linear

130 (ii) MOLECULE TYPE: protein

131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

132 Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu
133   1           5           10           15
134 Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro
135      20           25           30
136 Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
137      35           40           45
138 Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile
139      50           55           60
140 Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
141      65           70           75           80
142 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
143      85           90           95
144 Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu

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145           100           105           110
146 Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
147           115           120           125
148 Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
149           130           135           140
150 Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
151           145           150           155           160
152 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu
153           165           170           175
154 Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His
155           180           185           190
156 Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala
157           195           200           205
158 Leu Arg Gln Met
159           210

```

161 (2) INFORMATION FOR SEQ ID NO: 4:

162 (i) SEQUENCE CHARACTERISTICS:

163 (A) LENGTH: 211 amino acids

164 (B) TYPE: amino acid

165 (C) STRANDEDNESS:

166 (D) TOPOLOGY: linear

167 (ii) MOLECULE TYPE: protein

168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

169 Met Lys Phe Leu Ser Ala Arg Asp Phe His Pro Val Ala Phe Leu Gly
170 1           5           10           15
171 Leu Met Leu Val Thr Thr Thr Ala Phe Pro Thr Ser Gln Val Arg Arg
172           20           25           30
173 Gly Asp Phe Thr Glu Asp Thr Thr Pro Asn Arg Pro Val Tyr Thr Thr
174           35           40           45
175 Ser Gln Val Gly Gly Leu Ile Thr His Val Leu Trp Glu Ile Val Glu
176           50           55           60
177 Met Arg Lys Glu Leu Cys Asn Gly Asn Ser Asp Cys Met Asn Asn Asp
178           65           70           75           80
179 Asp Ala Leu Ala Glu Asn Asn Leu Lys Leu Pro Glu Ile Gln Arg Asn
180           85           90           95
181 Asp Gly Cys Tyr Gln Thr Gly Tyr Asn Gln Glu Ile Cys Leu Leu Lys
182           100          105          110
183 Ile Ser Ser Gly Leu Leu Glu Tyr His Ser Tyr Leu Glu Tyr Met Lys
184           115          120          125
185 Asn Asn Leu Lys Asp Asn Lys Lys Asp Lys Ala Arg Val Leu Gln Arg
186           130          135          140
187 Asp Thr Glu Thr Leu Ile His Ile Phe Asn Gln Glu Val Lys Asp Leu
188           145          150          155          160
189 His Lys Ile Val Leu Pro Thr Pro Ile Ser Asn Ala Leu Leu Thr Asp
190           165          170          175
191 Lys Leu Glu Ser Gln Lys Glu Trp Leu Arg Thr Lys Thr Ile Gln Phe
192           180          185          190
193 Ile Leu Lys Ser Leu Glu Glu Phe Leu Lys Val Thr Leu Arg Ser Thr
194           195          200          205

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195	Arg	Gln	Thr
196		210	

VERIFICATION SUMMARY

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L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:29 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:32 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:36 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]